Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L2	68	((alpha ADJ crystallin) OR (alpha ADJ A ADJ crystallin)) AND (435/69.1.ccls. OR 435/320.1.ccls. OR 530/350.ccls.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/25 13:09
L1	42330	435/69.1.ccls. OR 435/320.1.ccls. OR 530/350.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/25 13:09
S34	7	jaworski-c$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/25 09:36
S33	0	$jong-wilfried$.in.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:31
S32	958	$jong-w$.in.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:30
S31	11	pennings-j$.in.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:29
S30	0	pennings-jeroen$.in.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:29
S29	0	caspers-gert$.in.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:29
S27	205	(alpha ADJ crystallin) OR (alpha ADJ A ADJ crystallin)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:28
S26	3	smith-susan-m$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:25
S13	4779	smith-s$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:24

S25	2	koretz-jane-f$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:23
S14	4	koretz-j$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:23
S24	27	hanna-michael$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:22
S12	412	hanna-m$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:22
S23	10	salerno-john-c$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:21
S22	118	salerno-j$.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/06/24 15:21

119(e): Sept 6, 2002

=> d l5 ibib ti abs 1-8

L5 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:654757 CAPLUS
DOCUMENT NUMBER: 141:186716
TITLE: Sequence of truncated human α-crystallin and uses in expressing protein of interest
INVENTOR(S): Salerno, John C.; Hanna, Michael; Koretz, Jane F.; Crone, Donna; Smith, Susan M. E.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 33 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

current application

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004157289	A1	20040812	US 2003-657740		20030908
PRIORITY APPLN. INFO.:			US 2002-408680P	P	20020906

TI Sequence of truncated human α-crystallin and uses in expressing protein of interest

AB The present invention relates to a novel protein expression system having an oligonucleotide encoding a small heat shock protein (sHSP) operably linked to a promoter and an oligonucleotide encoding a protein of interest. In one embodiment the expressed sHSP is a **truncated** . **alpha.-crystallin** polypeptide, wherein the truncated sHSP lacks an N-terminal sequence present in the wild-type α-crystallin polypeptide. In an addnl. embodiment, a protein is coexpressed with a sHSP, thereby increasing the level of expression, enhancing folding and increasing the solubility of the protein. The invention further relates to protein and cDNA sequences of human α-crystallin.

L5 ANSWER 2 OF 8 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 1
ACCESSION NUMBER: 2005:166051 BIOSIS
DOCUMENT NUMBER: PREV200500165201
TITLE: Phosphoproteome analysis of hereditary cataractous rat lens alpha-crystallin.
AUTHOR(S): Kamei, Akira; Takamura, Shinsuke; Nagai, Makoto; Takeuchi, Noriko [Reprint Author]
CORPORATE SOURCE: Fac PharmBiochem SectTempa Ku, Meijo Univ, 150 Yagotoyama, Nagoya, Aichi, 4688503, Japan
ntakeuch@ccmfs.meijo-u.ac.jp
SOURCE: Biological & Pharmaceutical Bulletin, (December 2004) Vol. 27, No. 12, pp. 1923-1931. print.
ISSN: 0918-6158.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Apr 2005
Last Updated on STN: 27 Apr 2005

TI Phosphoproteome analysis of hereditary cataractous rat lens alpha-crystallin.

AB We reported previously that C-terminal **truncated alpha -crystallins** were found in lenses of hereditary cataractous rat ICR/f. In this study, we examined the phosphorylation of the crystalline lens proteins. alphabeta-crystallin and alphaA-crystallin, in cataractous and normal rats of different ages and have found an increase in the phosphorylation of serine residues of truncated a-crystallin in cataractous lens. Phosphorylation and C-terminal truncation of

alpha-crystallins could, both, reduce their chaperone-like activity and lead to cataract formation.

L5 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2004:262677 CAPLUS
DOCUMENT NUMBER: 140:373327
TITLE: C-terminal truncation of α-crystallin in hereditary cataractous rat lens
AUTHOR(S): Takeuchi, Noriko; Ouchida, Akie; Kamei, Akira
CORPORATE SOURCE: Section of Biochemistry, Faculty of Pharmacy, Meijo University, Nagoya, 468-8503, Japan
SOURCE: Biological & Pharmaceutical Bulletin (2004), 27(3), 308-314
CODEN: BPBLEO; ISSN: 0918-6158
PUBLISHER: Pharmaceutical Society of Japan
DOCUMENT TYPE: Journal
LANGUAGE: English
TI C-terminal truncation of α-crystallin in hereditary cataractous rat lens
AB C-Terminal **truncated** α -**crystallins** were found in lenses of hereditary cataractous rat ICR/f, including 2 truncated αB-crystallins and several truncated αA-crystallins. These truncated crystallins probably resulted from degradation by m-calpain and Lp82. The αB-crystallin with five amino acid residues deleted showed decreased chaperone activity. Compared with α-crystallins from the normal rat lenses, overall chaperone activity of α-crystallins from the mutant lenses, including the above truncated αB-crystallin, was remarkably reduced. The decreased chaperone activity accompanying the increase in C-terminal **truncated** . **alpha.-crystallins** may cause the insolubilization of many proteins in the mutant lenses, which it is likely to lead to the progression of cataract formation.
REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 8 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:529437 BIOSIS
DOCUMENT NUMBER: PREV200300525175
TITLE: SUSCEPTIBILITY OF OVINE LENS CRYSTALLINS TO PROTEOLYTIC CLEAVAGE BY CALPAIN DURING CATARACT FORMATION: A 2 - DE APPROACH.
AUTHOR(S): Robertson, L. J. G. [Reprint Author]; David, L. L.; Shearer, T. R.; Morton, J. D. [Reprint Author]; Bickerstaffe, R. [Reprint Author]
CORPORATE SOURCE: Animal and Food Sciences Division, Lincoln University, Christchurch, New Zealand
SOURCE: ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 2377. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003
TI SUSCEPTIBILITY OF OVINE LENS CRYSTALLINS TO PROTEOLYTIC CLEAVAGE BY CALPAIN DURING CATARACT FORMATION: A 2 - DE APPROACH.
AB Purpose: To identify and map crystallins in the normal ovine lens and to describe crystallin truncations. Truncations subsequently form during

cataractogenesis and may be attributed to ubiquitous calpain II and lens specific calpain Lp82. Methods: Two dimensional gel electrophoresis (2-DE) was performed on lens soluble and insoluble proteins from normal and cataractous sheep. Gels were stained, crystallin subunits were digested with trypsin within gel slices, and peptides were analysed by tandem mass spectrometry using electrospray ionization and an ion trap. Since there are no known sequences for ovine crystallins, proteins were identified by homology to the sequences of other mammalian crystallins. In the cataract lenses, the masses of **truncated alpha-crystallins** were determined by eluting the proteins from 2-DE gels and deconvoluting their electrospray ionization mass spectra. Results: A 2-DE map of ovine lens crystallins was created showing the normal complement of crystallins found in other mammals. Specific crystallin modifications were also noted, such as phosphorylation of alphaA-crystallin at residue 122. Insoluble ovine alphaA-crystallin, with a mass of 19,877, was extensively truncated in mature cataracts. Truncated species of ovine alphaA-crystallin with masses of 19,446 and 18,720 were observed. These decreases in mass were identical to the decreases observed in bovine and rat alphaA-crystallins after they were proteolyzed by calpain II and the lens specific calpain isoform Lp82. These truncated alphaA-crystallin species corresponded to masses expected when 5 or 11 residues were removed from the C-terminus by Lp82 and calpain II, respectively. This suggested that both Lp82 and calpain II were activated in ovine lenses developing mature cataracts. However, the 2-DE protein spot for the -5 Lp82 specific species was more abundant than the calpain II specific -11 species. Conclusion: Crystallins in the normal ovine lens appear similar to those of other mammals. Both calpain II and Lp82 cleavage sites on alpha-crystallin were found in the insoluble fraction of cataract lenses. However, the greater abundance of truncated alphaA-crystallin missing 5 residues from its C-terminus, suggested that Lp82 is preferentially activated in ovine lens. This data provides further support for calpain activation in the ovine cataract. It also provides the first evidence for increased Lp82 activation in a non-rodent species during cataract formation. These results require confirmation of Lp82 and calpain II cleavage sites on ovine crystallins in vitro.

L5 ANSWER 5 OF 8 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:529424 BIOSIS
DOCUMENT NUMBER: PREV200300525162
TITLE: LOCALIZATION OF a - CRYSTALLINS IN AGING NORMAL AND CATARACTOUS HUMAN LENSES.
AUTHOR(S): Harrington, V. R. [Reprint Author]; Srivastava, O. P. [Reprint Author]
CORPORATE SOURCE: Physiological Optics, Univ of Alabama at Birmingham, Birmingham, AL, USA
SOURCE: ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 2364. cd-rom. Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DOCUMENT TYPE: Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003
TI LOCALIZATION OF a - CRYSTALLINS IN AGING NORMAL AND CATARACTOUS HUMAN LENSES.
AB Purpose: The objective of this study was to determine the localization of **truncated alpha-crystallin** in aging human lenses and carry out comparative localization of the crystallin fragments

in normal and age-matched nuclear cataractous human lenses. Methods: Fresh 87-year-old normal and 79-year-old cataractous lenses were fixed, cryoprotected, and sectioned at 16 mum using the Leica 2800 E Friocut cryostat. The immunohistochemical analysis was done using two primary antibodies i.e., anti-alphaA-N-(residue nos. 1-9) antibody and anti-alphaA-C-(residue number 165-173) antibody. The secondary antibody was anti-rabbit IgG, made in goat and the fluorescent dye used for staining was Alexa 594 (red). Results: The results showed no difference in distribution of alphaA-crystallin in the central region on immunoreactivity with either anti-N-terminal or anti-C-terminal antibodies. The 87-year-old normal lens show a strong intense staining in the peripheral and bow regions with the anti-alphaA-N-antibody compared to the control. No such immunoreactivity with anti-alphaA-C antibody was observed. Similarly, the 79-year-old cataractous lens showed staining in the peripheral region only with the anti-alphaA-N-antibody. Conclusions: The lack of immunoreactivity with the anti-C-terminal antibody suggests loss of the C-terminal region in alphaA-crystallin in the peripheral region of both normal and cataractous lenses.

L5 ANSWER 6 OF 8 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 3

ACCESSION NUMBER: 2002:572650 BIOSIS
DOCUMENT NUMBER: PREV200200572650
TITLE: Enhanced C-terminal truncation of alphaA- and alphaB-crystallins in diabetic lenses.
AUTHOR(S): Thampi, Prajitha; Hassan, Azeem; Smith, Jean B.; Abraham, Edathara C. [Reprint author]
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Arkansas for Medical Sciences, 4301 West Markham Street, Slot 516, Little Rock, AR, 72205, USA abrahamedatharac@uams.edu
SOURCE: IOVS, (October, 2002) Vol. 43, No. 10, pp. 3265-3272. print.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 7 Nov 2002
Last Updated on STN: 7 Nov 2002

TI Enhanced C-terminal truncation of alphaA- and alphaB-crystallins in diabetic lenses.

AB Purpose. To investigate the influence of diabetes on the cleavage of C-terminal amino acid residues of alphaA- and alphaB-crystallins in human and rat lenses. Methods. The human lenses were diabetic or age-matched control lenses from donors 57, 59, 69, and 72 years of age. Lenses were also obtained from streptozotocin-induced diabetic rats. Individual lens crystallins in water-soluble fractions were separated by gel-permeation chromatography. The high (alphaH)- and low (alphaL)-molecular-weight fractions were analyzed by electrospray ionization mass spectrometry. Results. A typical mass spectrum of alphaA-crystallin from human lenses showed intact unmodified alphaA-crystallin, truncated alphaA1-172, and monophosphorylated alphaA-crystallin. Diabetic lenses showed nearly twofold higher levels of alphaA1-172 than did the control lenses. Also, the alphaH fraction consistently showed significantly higher levels of alphaA1-172 than the alphaL fraction. Human alphaB-crystallin showed no evidence of C-terminal truncation. Rat alphaA-crystallin had five C-terminal-truncated components, most of which showed substantial increases in diabetes. Truncated alphaA1-162 appeared only in the diabetic rat lenses, suggesting specific activation of m-calpain in diabetes. alphaB-crystallin had only one C-terminal-truncated component, alphaB1-170, which also showed increased levels in diabetes. Conclusions. These data suggest that diabetic stress causes either enzymatic or nonenzymatic cleavage of peptide bonds between specific C-terminal amino acid residues. Such **truncated alpha-**

crystallins appear to contribute to an increased level of the alphaH fraction generally present in diabetic lenses. Loss of alphaA-crystallin chaperone activity seems to be related to truncation of the C-terminal amino acid residues.

L5 ANSWER 7 OF 8 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 4
ACCESSION NUMBER: 2002:451132 BIOSIS
DOCUMENT NUMBER: PREV200200451132
TITLE: Mass measurements of C-terminally **truncated alpha-crystallins** from two-dimensional gels identify Lp82 as a major endopeptidase in rat lens.
AUTHOR(S): Ueda, Yoji; Fukiage, Chiho; Shih, Marjorie; Shearer, Thomas R.; David, Larry L. [Reprint author]
CORPORATE SOURCE: School of Dentistry and Medicine, Oregon Health and Science University, 611 S.W. Campus Dr., Portland, OR, 97201, USA davidl@ohsu.edu
SOURCE: Molecular and Cellular Proteomics, (May, 2002) Vol. 1, No. 5, pp. 357-365. print.
ISSN: 1535-9476.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 21 Aug 2002
Last Updated on STN: 21 Aug 2002

TI Mass measurements of C-terminally **truncated alpha-crystallins** from two-dimensional gels identify Lp82 as a major endopeptidase in rat lens.

AB Molecular chaperone activity of lens alpha-crystallins is reduced by loss of the C terminus. The purpose of this experiment was to 1) determine the cleavage sites produced in vitro by ubiquitous m-calpain and lens-specific Lp82 on alpha-crystallins, 2) identify alpha-crystallin cleavage sites produced in vivo during maturation and cataract formation in rat lens, and 3) estimate the relative activities of Lp82 and m-calpain by appearance of protease-specific cleavage products in vivo. Total soluble protein from young rat lens was incubated with recombinant m-calpain or Lp82 and 2 mM Ca2+. Resulting fragmented alpha-crystallins were separated by two-dimensional gel electrophoresis. Eluted alpha-crystallin spots were analyzed by mass spectrometry. Cleavage sites on insoluble alpha-crystallins were determined similarly in mature rat lens nucleus and in cataractous rat lens nucleus induced by selenite. In vitro proteolysis of alphaA-crystallin by Lp82 and m-calpain produced unique cleavage sites by removing 5 and 11 residues, respectively, from the C terminus. In vivo, the protease-specific truncations removing 5 and 11 residues from alphaA were both found in maturing lens, whereas only the truncation removing 5 residues was found in cataractous lens. Other truncation sites, common to both calpain isoforms, resulted from the removal of 8, 10, 16, 17, and 22 residues from the C terminus of alphaA. Using uniquely truncated alphaA-crystallins as in vivo markers, Lp82 and m-calpain were both found to be active during normal maturation of rat lens, whereas Lp82 seemed especially active during selenite cataract formation. These C-terminal truncations decrease chaperone activity of alpha-crystallins, possibly leading to the observed increases in insoluble proteins during aging and cataract. The methodology that allowed accurate mass measurements of proteins eluted from 2D gels should be useful to examine rapidly other post-translational modifications.

L5 ANSWER 8 OF 8 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 5
ACCESSION NUMBER: 93348329 EMBASE
DOCUMENT NUMBER: 1993348329
TITLE: High capacity binding of alpha crystallins to various bovine lens membrane preparations.

AUTHOR: Cenedella R.J.; Chandrasekher G.
CORPORATE SOURCE: Department of Biochemistry, Kirksville Coll Osteopathic Medicine, 800 W Jefferson Street,Kirksville, MO 65301, United States
SOURCE: Current Eye Research, (1993) Vol. 12, No. 11, pp. 1025-1038.
ISSN: 0271-3683 CODEN: CEYRDM
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 001 Anatomy, Anthropology, Embryology and Histology
012 Ophthalmology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 931226
Last Updated on STN: 931226

TI High capacity binding of alpha crystallins to various bovine lens membrane preparations.

AB This study examines the high capacity binding of intact and carboxyl-terminal-truncated alpha A(αA) crystallin to two types of lens membrane preparations; membrane stripped of extrinsic protein and some lipid by extraction with urea and alkali and unextracted membrane isolated by centrifugation of total water insoluble protein on a sucrose gradient (native membrane). High capacity binding of αA crystallin to the urea-treated membrane was seen once the αA substrate concentration reached about 1 mg/ml of media. The membrane bound up to one mg of αA per mg of intrinsic protein (MP26) at a concentration of 5 mg αA/ml media, binding 5 to 10 times greater than that seen by others at saturation of the high affinity but low capacity binding sites. No apparent differences were seen between high capacity binding of carboxyl terminal-truncated αA (by trypsin) and intact αA, although each crystallin could antagonize binding of the other. However, once membrane bound, neither crystallin appeared to grossly displace the other. Using the carboxyl terminal-**truncated alpha crystallin** as a model substrate, native membrane was seen to have a higher capacity to bind the **truncated alpha crystallin** than urea-extracted membrane and binding was better correlated with the preexisting αA content of the native membrane than its MP26 content. An artificial native membrane was prepared by prebinding the truncated αA to urea-extracted membrane. This preparation bound more intact αA than urea-extracted membrane bearing no prebound crystallin. We conclude that lens native membrane possesses a high capacity to bind alpha crystallins and that this binding could be mediated through protein-protein interactions with alpha crystallin bound in situ to the membrane as extrinsic protein.

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FULL ESTIMATED COST	35.21	36.60

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DICTIONARY FILE UPDATES: 24 JUN 2005 HIGHEST RN 852980-90-6

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information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html

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=> s 158856-54-3/rn
L6            1 158856-54-3/RN

=> d l6

L6   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2005 ACS on STN
RN   158856-54-3  REGISTRY
ED   Entered STN:  10 Nov 1994
CN   α-Crystallin (human A-chain reduced) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   αA-Crystallin (CRYA1) (human clone KB2007G4 gene CRYAA)
CN   αA-Crystallin (human eye lens)
CN   Crystallin, αA- (human 173-amino acids)
FS   PROTEIN SEQUENCE
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS, TOXCENTER

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               5 REFERENCES IN FILE CAPLUS (1907 TO DATE)


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FULL ESTIMATED COST                               2.27      38.87

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                                                 ENTRY    SESSION
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FILE COVERS 1907 - 25 Jun 2005 VOL 143 ISS 1
FILE LAST UPDATED: 24 Jun 2005 (20050624/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s l6
L7 5 L6

=> d l7 ibib ti abs 1-5

L7 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2000:366621 CAPLUS
DOCUMENT NUMBER: 132:344010
TITLE: The DNA sequence of human chromosome 21
AUTHOR(S): Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.; Park, H.-S.; Toyoda, A.; Ishil, K.; Totoki, Y.; Choi, D.-K.; Soeda, E.; Ohki, M.; Takagi, T.; Sakaki, Y.; Taudlen, S.; Blechschmidt, K.; Polley, A.; Menzel, U.; Delabar, J.; Kumpf, K.; Lehmann, R.; Patterson, D.; Reichwald, K.; Rump, A.; Schillhabel, M.; Schudy, A.; Zimmermann, W.; Rosenthal, A.; Kudoh, J.; Shibuya, K.; Kawasaki, K.; Asakawa, S.; Shintani, A.; Sasaki, T.; Nagamine, K.; Mitsuyama, S.; Antonarakis, S. E.; Minoshima, S.; Shimizu, N.; Nordsiek, G.; Hornischer, K.; Brandt, P.; Scharfe, M.; Schon, O.; Desario, A.; Reichelt, J.; Kauer, G.; Blocker, H.; Ramser, J.; Beck, A.; Klages, S.; Hennig, S.; Riesselmann, L.; Dagand, E.; Haaf, T.; Wehrmeyer, S.; Borzym, K.; Gardiner, K.; Nizetic, D.; Francis, F.; Lehrach, H.; Reinhardt, R.; Yaspo, M.-L.
CORPORATE SOURCE: Genomic Sciences Center, RIKEN, Sagamihara, 228-8555, Japan
SOURCE: Nature (London) (2000), 405(6784), 311-319
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
TI The DNA sequence of human chromosome 21
AB Chromosome 21 is the smallest human autosome. An extra copy of chromosome 21 causes Down syndrome, the most frequent genetic cause of significant mental retardation, which affects up to 1 in 700 live births. Several

anonymous loci for monogenic disorders and predispositions for common complex disorders have also been mapped to this chromosome, and loss of heterozygosity has been observed in regions associated with solid tumors. This report provides the sequence and gene catalog of the long arm of chromosome 21. At least 33,546,361 base pairs (bp) of DNA have been sequenced with very high accuracy, the largest contig being 25,491,867 bp. Only 3 small clone gaps and 7 sequencing gaps remain, comprising .apprx.100 kilobases. Thus, 99.7% coverage of 21q was achieved. About 281,116 bp were also sequenced from the short arm. The structural features identified include duplications that are probably involved in chromosomal abnormalities and repeat structures in the telomeric and pericentromeric regions. Anal. of the chromosome revealed 127 known genes, 98 predicted genes and 59 pseudogenes. The sequences are deposited in the GenBank database, and addnl. information can be sound from the home pages of the participating centers of the chromosome 21 sequencing consortium.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1997:21633 CAPLUS
DOCUMENT NUMBER: 126:141113
TITLE: Cloning, expression, and chaperone-like activity of human αA-crystallin
AUTHOR(S): Andley, Usha P.; Mathur, Shashank; Griest, Terry A.; Petrash, J. Mark
CORPORATE SOURCE: Dep. Ophthalmol. Visual Sci., Washington Univ. Sch. Med., St. Louis, MO, 63110, USA
SOURCE: Journal of Biological Chemistry (1996), 271(50), 31973-31980
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

TI Cloning, expression, and chaperone-like activity of human αA-crystallin

AB One of the major protein components of the ocular lens, α-crystallin, is composed of αA and αB chain subunits that have structural homol. to the family of mammalian small heat shock proteins. Like other small heat shock proteins, α-crystallin subunits associate to form large oligomeric aggregates that express chaperone-like activity, as defined by the ability to suppress nonspecific aggregation of proteins destabilized by treatment with a variety of denaturants including heat, UV irradiation, and chemical modification. It has been proposed that age-related loss of sequences at the C terminus of the αA chain subunit may be a factor in the pathogenesis of cataract due to diminished capacity of the truncated crystallin to protect against nonspecific aggregation of lens proteins. To evaluate the functional consequences of α-crystallin modification, two mutant forms of αA subunits were prepared by site-directed mutagenesis. Like wild type (WT), aggregates of .apprx.540 kDa were formed from a tryptophan-free αA mutant (W9F). When added in stoichiometric amts., both WT and W9F subunits completely suppressed the heat-induced aggregation of aldose reductase. In contrast, subunits encoded by a truncation mutant in which the C-terminal 17 residues were deleted (R157STOP), despite having spectroscopic properties similar to WT, formed much larger aggregates with a marked reduction in chaperone-like activity. Similar results were observed when the chaperone-like activity was assessed through inhibition of γ-crystallin aggregation induced by singlet oxygen. These results demonstrate that the structurally conservative substitution of Phe for Trp-9 has a negligible effect on the functional interaction of αA

subunits, and that deletion of C-terminal sequences from the αA subunit results in substantial loss of chaperone-like activity, despite overall preservation of secondary structure.

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1997:608 CAPLUS
DOCUMENT NUMBER: 126:102492
TITLE: Modifications of the water-insoluble human lens α-crystallins
AUTHOR(S): Lund, Anders L.; Smith, Jean B.; Smith, David L.
CORPORATE SOURCE: Dep. Chem., Univ. Nebraska, Lincoln, NE, 68588-0304, USA
SOURCE: Experimental Eye Research (1996), 63(6), 661-672
CODEN: EXERA6; ISSN: 0014-4835
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

TI Modifications of the water-insoluble human lens α-crystallins

AB Since the water-insol. crystallins of the lens may be the precursors of cataract, identifying the modifications that differentiate the water-insol. from the water-soluble crystallins may provide the basis for understanding the chemical leading to cataract. This investigation of the α-crystallins of the water-insol. urea-soluble portion of 45-yr-old normal clear lenses, isolated using gel filtration, ion exchange and reversed phase chromatog., has employed state-of-the-art mass spectrometric techniques to identify and locate the modifications of the water-insol. α-crystallins. Modifications present in the isolated α-crystallins were identified by the mol. wts. of the modified proteins, by the mol. wts. of peptides produced by enzymic digestion of the proteins, and by the fragmentation patterns produced by collisional activation of the peptides. Modifications that are either unique to the water-insol. α-crystallins or are more prevalent in the water-insol. portion than in the water-soluble part include complete oxidation of the two Cys residues of αA-crystallin to form an intramol. disulfide bond, partial truncation at both the C-termini and N-termini of αA- and αB-crystallins, partial oxidation of Met residues to methionine sulfoxide, partial deamidation of several Asn and Gln residues, and evidence of peptide bond cleavage at some of the deamidated residues. Although many reactions have been proposed to contribute to the insoly. of crystallins, this compilation of in vivo post-translational modifications of water-insol. α-crystallins delineates products that are actually present at levels of 5% or more. From these results, it is hypothesized that α-crystallin becomes water-insol. following deamidation of various Asn and Gln residues which cause conformational changes leading to formation of an intra-mol. disulfide bond between the Cys residues of αA-crystallin.

L7 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1996:29717 CAPLUS
DOCUMENT NUMBER: 124:280515
TITLE: A reassessment of mammalian αA-crystallin sequences using DNA sequencing: implications for anthropoid affinities of tarsier
AUTHOR(S): Jaworski, Cynthia J.
CORPORATE SOURCE: Lab. Mol. Developmental Biol., Natl. Eye Inst., Bethesda, MD, 28092, USA
SOURCE: Journal of Molecular Evolution (1995), 41(6), 901-8
CODEN: JMEVAU; ISSN: 0022-2844
PUBLISHER: Springer

DOCUMENT TYPE: Journal
LANGUAGE: English

TI A reassessment of mammalian αA-crystallin sequences using DNA sequencing: implications for anthropoid affinities of tarsier

AB αA-crystallin, a major structural protein in the ocular lenses of all vertebrates, has been a valuable tool for mol. phylogenetic studies. This paper presents the complete sequence for human αA-crystallin derived from cDNA and genomic clones. The deduced amino acid sequence differs at two phylogenetically informative positions from that previously inferred from peptide composition This led us to examine the same region of the αA-crystallin gene in 12 other mammalian species using direct sequencing of PCR-amplified genomic DNA. New sequences were added to the database, and corrections were made to all anthropoid sequences, defining clear synapomorphies for anthropoids as a clade distinct from prosimians. Within the anthropoids there are further synapomorphies delineating hominoids, Old World monkeys, and New World monkeys. Significantly, sequence revisions and the addition of new sequence for a prosimian, the sifaka, eliminate the previous support for the proposed anthropoid affinities of the tarsier inferred from αA-crystallin protein sequences. In addition, DNA sequences provide greater resolution of certain relationships. For example, although they are identical in protein sequence, comparison of DNA sequences clearly separates mouse and the common tree shrew, grouping the tree shrew closer to prosimians. These results show that adding DNA sequences to the existing αA-crystallin database can enhance its value in resolving phylogenetic relationships.

L7 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1994:673440 CAPLUS
DOCUMENT NUMBER: 121:273440
TITLE: A partial cDNA sequence corrects the human αA-crystallin primary structure
AUTHOR(S): Caspers, Gert-Jan; Pennings, Jeroen; De Jong, Wilfried W.
CORPORATE SOURCE: Dep. Biochem., Univ. Nijmegen, Nijmegen, 6500 HB, Neth.
SOURCE: Experimental Eye Research (1994), 59(1), 125-6
CODEN: EXERA6; ISSN: 0014-4835
DOCUMENT TYPE: Journal
LANGUAGE: English

102(b) art.

TI A partial cDNA sequence corrects the human αA-crystallin primary structure

AB The primary structure of the human αA-crystallin chain was proposed almost 20 yr ago, on the basis of peptide compns. and partial Edman degradation (de Jong et al., 1975; Kramps et al., 1978). With the advent of the DNA era, the largest part of the amino acid sequence was fully confirmed by deduction from the DNA sequences of the first two exons and the 3' end of the third exon of the human αA-crystallin gene (McDevitt et al., 1986; Jaworski and Piatigorsky, 1989). The DNA sequence of the larger part of the third exon, corresponding to positions 105-165 in the 173-residue αA-crystallin chain, still remained undetd. During the course of comparative studies of the αA-crystallin sequences of different animals, we designed two degenerate oligonucleotide primers, encompassing a region coding for amino acids 74-160. These primers were used to amplify a partial αA-crystallin cDNA sequence from a human lens cDNA library in phage λgt11 by the polymerase chain reaction (PCR) method (Saiki et al., 1985). PCR products were cloned and the sequence was determined by the dideoxynucleotide chain-termination method. The part of the nucleotide sequence of the human αA-crystallin cDNA that codes for amino acids 105-160 and its derived amino acid sequence were determined

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               356   FILE PASCAL
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L1               QUE ALPHA CRYSTALLIN
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L4            21 S TRUNCATED ALPHA CRYSTALLIN
L5             8 DUP REM L4 (13 DUPLICATES REMOVED)

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L7             5 S L6

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